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TUMOR SUPPRESSOR MOLECULES AND METHODS OF USE

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Peter J. Welch
and
Jack R. Barber

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Attorneys

CAMPBELL & FLORES LLP
4370 La Jolla Village Drive, Suite 700
San Diego, California 92122

TUMOR SUPPRESSOR MOLECULES AND METHODS OF USE

BACKGROUND OF THE INVENTION

This invention relates generally to proliferative diseases such as cancer and, more specifically, to tumor suppressor molecules that can be used to diagnose and treat proliferative diseases.

Cancer is one of the leading causes of death in the United States. Each year, more than half a million Americans die from cancer, and more than one million are newly diagnosed with the disease. Cancerous tumors result when a cell escapes from its normal growth regulatory mechanisms and proliferates in an uncontrolled fashion. Tumor cells can metastasize to secondary sites if treatment of the primary tumor is either not complete or not initiated before substantial progression of the disease. Early diagnosis and effective treatment of tumors is therefore essential for survival.

Cancer involves the clonal replication of populations of cells that have gained competitive advantage over normal cells through the alteration of regulatory genes. Regulatory genes can be broadly classified into "oncogenes" which, when activated or overexpressed promote unregulated cell proliferation, and "tumor suppressor genes" which, when inactivated or underexpressed fail to prevent abnormal cell proliferation. Loss of function or inactivation of tumor suppressor genes is thought to play a central role in the initiation and progression of a significant number of human cancers.

A number of tumor suppressor genes have been identified that, when inactivated, are involved in the initiation or progression of human cancers. Known tumor suppressor genes include, for example, RB, p53, DCC, APC/MCC, NF1, NF2, WT1, VHL, BRCA1, MST1 and WAF1/CIP1. Approaches for treating cancer by modulating the function of certain of these tumor suppressor genes, either with pharmaceutical compounds or by gene therapy methods, have yielded promising results in animal models and in human clinical trials.

Approaches for diagnosing and prognosing cancer by identifying mutations in known tumor suppressor genes have also been developed. For example, identifying individuals containing germline mutations in known tumor suppressor genes has permitted the identification of individuals at increased risk of developing cancer. Such individuals are then closely monitored or treated prophylactically to improve their chance of survival. Identifying the pattern of alterations of known tumor suppressor genes in biopsy samples is also being used to determine the presence or stage of a tumor. Being able to determine whether a cancer is benign or malignant, at an early or late stage of progression, provides the patient and clinician with a more accurate prognosis and can be used to determine the most effective treatment.

In view of the importance of tumor suppressor molecules in the detection and treatment of cancer, there exists a need to identify additional tumor suppressor nucleic acids and polypeptides. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF INVENTION

The invention provides substantially pure tumor suppressor nucleic acid molecules. In one embodiment, the invention provides a substantially pure tumor suppressor nucleic acid molecule having at least fifteen contiguous nucleotides of SEQ ID NO:2, or a functional fragment thereof. In another embodiment, the invention provides a substantially pure nucleic acid molecule having substantially the same nucleic acid sequence as SEQ ID NO:5, or a functional fragment thereof. In yet another embodiment, the invention provides a substantially pure tumor suppressor nucleic acid molecule having at least fifteen contiguous nucleotides of SEQ ID NO:4, or a functional fragment thereof.

The invention also provides substantially pure hairpin ribozyme nucleic acid molecules, containing a sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:3.

The invention further provides a substantially pure tumor suppressor polypeptide having substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof. A substantially pure antibody or antigen binding fragment reactive with the tumor suppressor polypeptide is also provided.

Also provided are methods of detecting a neoplastic cell in a sample. In one embodiment, the method consists of contacting the sample with a detectable agent specific for a tumor suppressor nucleic acid of the invention and detecting the nucleic acid molecule in the sample, wherein altered expression or

structure of the nucleic acid molecule indicates the presence of a neoplastic cell in said sample. In another embodiment, the method consists of contacting the sample with a detectable agent specific for a tumor suppressor polypeptide of the invention and detecting the polypeptide in the sample, wherein altered expression or structure of the polypeptide indicates the presence of a neoplastic cell in the sample.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A shows the general structure and nucleotide sequence of a hairpin ribozyme (SEQ ID NO:10) and its interaction with a substrate RNA. Figure 1B shows the pLHPM retroviral vector used to clone the ribozyme gene library.

Figure 2 shows soft agar colonies formed in HF cells stably transfected with ribozyme 568 (Rz 568), or its disabled counterpart, d568, after two rounds of soft agar selection.

Figure 3A shows the relative level of HTS1 (hPPAN) mRNA in HF parental cells, Hela cells, and HF cells expressing either CNR3 (control), 568 or d568 ribozymes.

Figure 3B shows an alignment of HTS1 (Hs) amino acid sequence with PPAN sequences from *Drosophila* (Dm) (SEQ ID NO:17) and deduced from Mouse (Mm) (SEQ ID NO:16).

Figure 4A shows soft agar colonies formed after two rounds of selection in HF cells stably transfected with the indicated target validation (TV) ribozyme

expression constructs or a control Rz against HIV. Figure 4B shows Northern blot analysis of HTS1 (hPPAN) mRNA levels relative to G3PDH mRNA in cells expressing target validation Rz or control Rz.

Figure 5 shows colonies of Hela and HF cells formed after transfecting cells with HTS1 (hPPAN) or a frameshift mutant (FS) in pIRES-Hyg vector, or vector control, followed by two weeks of hygromycin selection.

Figure 6A shows the nucleotide sequence (SEQ ID NO:5) and Figure 6B shows the amino acid sequence (SEQ ID NO:6) of the human tumor suppressor molecule designated HTS1.

Figure 7 shows a deduced partial amino acid sequence of mouse PPAN (MM; SEQ ID NO:19) and human PPAN (HS; SEQ ID NO:20) compiled from ESTs, as set forth in Figure 4 of Migeon et al., Mol. Biol. Cell. 10:1733-1744 (1999).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel tumor suppressor molecules, including tumor suppressor nucleic acids and polypeptides. The tumor suppressor molecules of the invention can be used to detect neoplastic cells in a sample and, therefore, to diagnose and prognose cancer. The tumor suppressor molecules of the invention can also be introduced into neoplastic cells to regulate cell proliferation and, therefore, are useful as therapeutics for treating cancer. Furthermore, the tumor suppressor molecules of the invention can be used to identify compounds that mimic or regulate their tumor

suppressor activity. Such compounds can be used as therapeutics to treat cancer.

As used herein, the term "tumor suppressor" when used in reference to a nucleic acid molecule or polypeptide is intended to mean either a nucleic acid molecule, or an encoded polypeptide which, when functionally inactivated in a cell, promotes unregulated cell proliferation. As described herein, one method of functionally inactivating a tumor suppressor nucleic acid molecule in a cell is by introducing into the cell a gene for a hairpin ribozyme with specificity for the tumor suppressor nucleic acid molecule. The hairpin riboyzme binds the specific target site in the cellular mRNA and cleaves the transcript, preventing the expression of a functional tumor suppressor polypeptide. Those skilled in the art will appreciate that expression of an active tumor suppressor molecule in a cell, particularly in a cell in which the endogenous tumor suppressor molecule has been functionally inactivated, can confer, to some extent, normal regulatory properties on the cell.

As used herein, the term "substantially pure," in regard to a nucleic acid molecule or polypeptide of the invention, is intended to mean a molecule that is substantially free from cellular components or other contaminants that are not the desired molecule. A substantially pure nucleic acid molecule or polypeptide will generally resolve as a major band by gel electrophoresis, and will generate a nucleotide or amino acid sequence profile consistent with a predominant species.

As used herein, the term "nucleic acid molecule" is intended to mean a single- or double-stranded DNA or RNA molecule. Thus, a nucleotide designated as "T" is equivalent to a "U" nucleotide in a recited sequence. The term is intended to include nucleic acid molecules of both synthetic and natural origin. A nucleic acid molecule of natural origin can be derived from any animal, such as a human, non-human primate, mouse, rat, rabbit, bovine, porcine, ovine, canine, feline, or amphibian. A nucleic acid molecule of the invention can be of linear, circular or branched configuration, and can represent either the sense or antisense strand, or both, of a native nucleic acid molecule. A nucleic acid molecule of the invention can further incorporate a detectable moiety such as a radiolabel, a fluorochrome, a ferromagnetic substance, a luminescent tag or a detectable binding agent such as biotin, when used in a diagnostic method described herein. Additionally, a nucleic acid molecule of the invention can include one or more non-native nucleotides, having, for example, modifications to the base, the sugar, or the phosphate portion, or having a modified phosphodiester linkage. Such modifications can be advantageous in increasing the stability of the nucleic acid molecule.

As used herein, the term "functional fragment," in regard to a nucleic acid molecule of the invention refers to a portion of the nucleic acid molecule having the ability to selectively hybridize with the subject nucleic acid molecule. The term "selectively hybridize" refers to an ability to bind the subject nucleic acid molecule without substantial cross-reactivity with a molecule that is not the subject nucleic acid molecule. Thus, a functional fragment of a nucleic acid molecule of

the invention can be used, for example, as a PCR primer to selectively amplify a nucleic acid molecule of the invention; as a selective primer for 5' or 3' RACE to determine additional 5' or 3' sequence of a nucleic acid molecule of the invention; as a selective probe to identify or isolate a nucleic acid molecule of the invention on a Northern or Southern blot, or genomic or cDNA library; or as a selective inhibitor of transcription or translation of a tumor suppressor nucleic acid in a cell or cell extract.

A functional fragment of a nucleic acid molecule of the invention includes at least 15 contiguous nucleotides from the reference nucleic acid molecule, can include at least 16, 17, 18, 19, 20 or at least 25 nucleotides, often includes at least 30, 40, 50, 75, 100, 200, 300, 400, 500, 600, 800, 1000 nucleotides, and can include up to the full length of the reference nucleic acid molecule minus one nucleotide. Functional fragments of such lengths are able to selectively hybridize with the subject nucleic acid molecule in a variety of detection formats described herein.

As used herein, the term "substantially the same nucleotide sequence" in reference to a nucleic acid molecule of the invention or a fragment thereof includes sequences having one or more additions, deletions or substitutions with respect to the reference sequence, so long as the nucleic acid molecule retains its ability to selectively hybridize with the subject nucleic acid molecule under moderately stringent conditions, or highly stringent conditions. The term "moderately stringent conditions," as used herein, refers to hybridization conditions equivalent to hybridization of filter-bound nucleic acid in 50% formamide, 5 X Denhart's solution, 5

X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2 X SSPE, 0.2% SDS, at 50°. As used herein, "highly stringent conditions" are conditions equivalent to hybridization of filter-bound nucleic acid in 50% formamide, 5 X Denhart's solution, 5 X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2 X SSPE, 0.2% SDS, at 65°. Other suitable moderately stringent and highly stringent hybridization buffers and conditions are well known to those of skill in the art and are described, for example, in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1992) and in Ansubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, MD (1998).

In general, a nucleic acid molecule that has "substantially the same nucleotide sequence" as a reference sequence will have greater than about 60% identity, such as greater than about 65%, 70%, 75% identity with the reference sequence, such as greater than about 80%, 85%, 90%, 95%, 97% or 99% identity to the reference sequence over the length of the two sequences being compared. Identity of any two nucleic acid sequences can be determined by those skilled in the art based, for example, on a BLAST 2.0 computer alignment, using default parameters. BLAST 2.0 searching is available at http://www.ncbi.nlm.nih.gov/gorf/bl2.html., as described by Tatiana et al., FEMS Microbiol Lett. 174:247-250 (1999).

As used herein, the term "nucleic acid molecule encoding an amino acid sequence" is intended to mean a nucleic acid molecule that encodes the reference amino acid sequence, yet can be degenerate at one or several codons with respect to the native nucleotide sequence.

As used herein, the term "substantially the same amino acid sequence" is intended to mean an amino acid sequence that contains minor modifications with respect to the reference amino acid sequence, so long as the polypeptide retains one or more of the functional activities exhibited by the polypeptide as a whole. A polypeptide that has substantially the same amino acid sequence as a reference human amino acid sequence can be, for example, a homologous polypeptide from a vertebrate species, such as a non-human primate, mouse, rat, rabbit, bovine, porcine, ovine, canine, feline, or amphibian.

A polypeptide that has substantially the same amino acid sequence as a reference sequence can also have one or more deliberately introduced modifications, such as additions, deletions or substitutions of natural or non-natural amino acids, with respect to the reference sequence. Those skilled in the art can determine appropriate modifications that, for instance, serve to increase the stability, bioavailability, bioactivity or immungenicity of the polypeptide, or facilitate its purification, without altering the desired functional acitivity. For example, introduction of a D-amino acid or an amino acid analog, or deletion of a lysine residue, can stabilize a polypeptide and reduce degradation. Likewise, addition of tag sequeces, such as epitope or histidine tags, or sorting sequences, can facilitate purification of the recombinant polypeptide. Depending on the modification and the source of the polypeptide, the modification can be introduced into the polypeptide, or into the encoding nucleic acid sequence.

Computer programs known in the art, for example, DNASTAR software, can be used to determine which amino acid residues can be modified as indicated above

without abolishing the desired functional activity. Additionally, guidance in modifying amino acid sequences while retaining functional activity is provided by aligning homologous tumor suppressor polypeptides from various species. Those skilled in the art understand that evolutionarily conserved amino acid residues and domains are more likely to play a role in the biological activity than less well-conserved residues and domains.

In general, an amino acid sequence that is substantially the same as a reference amino acid sequence will have greater than about 50% identity, preferably greater than about 60% identity, such as greater than about 70%, 75%, or about 80% identity, more preferably greater than about 85% or 90% identity, including greater than about 95%, 97% or 99% identity with the reference sequence. The amino acid sequences which align across two sequences, and the presence of gaps and non-homologous regions in the alignment, can be determined by those skilled in the art based, for example, on a BLAST 2 or Clustal W or similar computer alignment, using default parameters.

A computer alignment can, if desired, be optimized visually by those skilled in the art. The percent identity of two sequences is determined as the percentage of the total amino acids that align in such an alignment which are identical. Those skilled in the art understand that two amino acid molecules with a given percentage identity over the entire sequence or over a substantial portion or portions thereof, are more likely to exhibit similar functional activities than two molecules with the same percentage identity over a shorter portion of the sequence.

As used herein, the term "functional activity" of a polypeptide of the invention is an activity which is characteristic of the reference polypeptide. A functional activity can be, for example, immunogenicity, which is an ability to generate an antibody that selectively binds a polypeptide of the invention, or antigenicity, which is an ability to selectively compete with a polypeptide of the invention for binding to an antibody specific for a polypeptide of the invention. A "functional activity" of a tumor suppressor polypeptide of the invention can additionally or alternatively be the ability to alter, such as inhibit or promote, cell proliferation, when introduced or expressed in a cell. Such a functional activity reflects the ability of the polypeptide to either mimic or compete with the endogenous tumor suppressor polypeptide, as described below.

As used herein, the term "functional fragment" in regard to a polypeptide of the invention, refers to a portion of the reference polypeptide that is capable of exhibiting or carrying out a "functional activity" of the reference polypeptide. A functional fragment of a polypeptide of the invention exhibiting a functional activity can have, for example, at least 6 contiguous amino acid residues from the polypeptide, at least 8, 10, 15, 20, 30 or 40 amino acids, and often has at least 50, 75, 100, 200, 300, 400 or more amino acids of a polypeptide of the invention, up to the full length polypeptide minus one amino acid.

The appropriate length and amino acid sequence of a functional fragment of a polypeptide of the invention can be determined by those skilled in the art, depending on the intended use of the functional fragment.

For example, a functional fragment having immunogenic or antigenic activity need only be of sufficient length to define an epitope that is specific for the polypeptide of the invention. A functional fragment that alters cell proliferation by competing with an endogenous tumor suppressor can be chosen, for example, to correspond to a portion of the polypeptide that includes the region that interacts with a substrate or regulatory molecule. A functional fragment that mimics an endogenous tumor suppressor can include, for example, an entire biologically active domain of the tumor suppressor molecule.

As used herein, the term "hairpin ribozyme" is intended to mean an RNA molecule having the general nucleic acid sequence and two-dimensional configuration of the molecule shown in Figure 1 (SEQ ID NO:10), and which is capable of selectively binding, or of both selectively binding and cleaving, a substrate RNA. Usually, a hairpin ribozyme will have from about 50 to 54 nucleotides, and forms two helical domains (Helix 3 and Helix 4) and 3 loops (Loops 2, 3 and 4). Two additional helices, Helix 1 and Helix 2, form between the ribozyme and its RNA substrate. A hairpin ribozyme binds a target RNA substrate by forming Watson-Crick base pairs between the substrate and Helix 1 and Helix 2 sequences, as shown by dots in Figure 1, where "N" is any nucleotide, "n" is the complement of "N", "b" is generally C, G or U, and "B" is the complement of "b". The length of Helix 2 is usually 4 base pairs, and the length of Helix 1 can vary from about 6 to about 10 base pairs. A hairpin ribozyme can have catalytic activity, and thus cleave the substrate RNA at the indicated cleavage site in Figure 1. However, the catalytic activity of the hairpin ribozyme can be disabled by altering the AAA sequence in Loop 2 to

CGU, as shown in Figure 2. Those skilled in the art can determine which modifications to the overall hairpin ribozyme structure can be made and still maintain the substrate binding, or both substrate binding and catalytic activity, of a hairpin ribozyme of the invention.

As used herein, the term "hairpin ribozyme nucleic acid molecule" includes both hairpin ribozyme RNA molecules as well as single- and double-stranded DNA molecules that, when expressed, form hairpin ribozyme RNA molecules.

As used herein, the term "specifically reactive" in relation to an HTS1 antibody or other binding compound, is intended to mean high affinity binding to HTS1 in a binding assay, such as an immunoblot or ELISA assay, without substantial cross-reactivity with other polypeptides. A specifically reactive antibody or other binding compound can have an affinity constant of greater than 10^5 M^{-1}, preferably greater than 10^7 M^{-1}, more preferably greater than 10^9 M^{-1}, for HTS1 or a characteristic fragment therefrom.

As used herein, the term "neoplastic cell" is intended to mean a cell that has altered expression or structure of a tumor suppressor molecule of the invention compared to a normal cell from the same or a different individual. A neoplastic cell will generally also exhibit histological or proliferative features of a malignant or premalignant cell. For example, by histological methods, a neoplastic cell can be observed to invade into surrounding normal tissue, have an increased mitotic index, an increased nuclear to cytoplasmic ratio, altered deposition of extracellular

matrix, or a less differentiated phenotype. A neoplastic cell can also exhibit unregulated proliferation, such as anchorage independent cell growth, proliferation in reduced-serum medium, loss of contact inhibition, or rapid proliferation compared to normal cells.

As used herein, the term "altered expression" of a nucleic acid molecule detected by a method of the invention refers to an increased or decreased amount of a tumor suppressor nucleic acid in the test sample relative to known levels in a normal sample. Altered abundance of a nucleic acid molecule can result, for example, from an altered rate of transcription, from altered transcript stability, or from altered copy number of the corresponding gene.

As used herein, the term "altered structure" of a nucleic acid molecule refers to differences, such as point mutations, deletions, translocations, splice variations and other rearrangements, between the structure of a nucleic acid molecule of the invention in a test sample and the structure of the nucleic acid molecule in a normal sample. Those skilled in the art understand that mutations that alter the structure of a nucleic acid molecule can also alter its expression.

As used herein, the term "altered expression" of a polypeptide refers to an increased or decreased amount, or altered subcellular localization, of the polypeptide in the test sample relative to known levels or localization in a normal sample. Altered abundance of a polypeptide can result, for example, from an altered rate of translation or altered copy number of the corresponding message, or from altered stability of the protein. Altered subcellular localization can result,

for example, from truncation or inactivation of a sorting sequence, from fusion with another polypeptide sequence, or altered interaction with other celllular polypeptides.

As used herein, the term "altered structure" of a polypeptide refers to differences in amino acid sequence, post-translational modifications, or conformation, of the polypeptide in the test sample relative to a normal sample. Post-translational modifications include, for example, phosphorylation, glycosylation and acylation. Conformational differences include, for example, folding properties. Such differences can be detected, for example, with a structure-specific detectable binding agent.

As used herein, the term "sample" is intended to mean any biological fluid, cell, tissue, organ or portion thereof, that includes or potentially includes nucleic acids and polypeptides of the invention. The term includes samples present in an individual as well as samples obtained or derived from the individual. For example, a sample can be a histologic section of a specimen obtained by biopsy, or cells that are placed in or adapted to tissue culture. A sample further can be a subcellular fraction or extract, or a crude or substantially pure nucleic acid or protein preparation. A sample can be prepared by methods known in the art suitable for the particular format of the detection method.

As used herein, the term "detectable agent" refers to a molecule that renders a tumor suppressor molecule of the invention detectable by an analytical method. An appropriate detectable agent depends on the particular detection format, and can be determined for a

particular application of the method by those skilled in the art. For example, a detetable agent specific for a tumor suppressor nucleic acid molecule can be a complementary nucleic acid molecule, such as a hybridization probe or non-catalytic ribozyme, that selectively hybridizes to the nucleic acid molecule. A hybridization probe or ribozyme can be labeled with a detectable moiety, such as a radioisotope, fluorochrome, chemiluminescent marker, biotin, or other detectable moiety known in the art that is detectable by analytical methods.

A detectable agent specific for a tumor suppressor nucleic acid molecule can also be, for example, a PCR or RT-PCR primer, which can be used to selectively amplify all or a desired portion of the nucleic acid molecule, which can then be detected by methods known in the art. Furthermore, a detectable agent specific for a tumor suppressor nucleic acid molecule can be a selective binding agent, such as a peptide, nucleic acid analog, or small organic molecule, identified, for example, by affinity screening of a library of compounds.

A detectable agent specific for a polypeptide of the invention can be, for example, an agent that selectively binds the polypeptide. For example, a detectable agent that detects a polypeptide can selectively bind with high affinity or avidity to the polypeptide, without substantial cross-reactivity with other polypeptides that are not polypeptides of the invention. The binding affinity of a detectable agent that selectively binds a polypeptide will generally be greater than about 10^{-5} M and more preferably greater than about 10^{-6} M for the polypeptide. High affinity

interactions are preferred, and will generally be greater than about 10^{-8} M to 10^{-9} M.

A detectable agent specific for a polypeptide can be, for example, a polyclonal or monoclonal antibody specific for the polypeptide, or other selective binding agent identified, for example, by affinity screening of a library of compounds. For certain applications, a detectable agent can be utilized that preferentially recognizes a particular conformational or post-translationally modified state of the polypeptide. The detectable agent can be labeled with a detectable moiety, if desired, or rendered detectable by specific binding to a detectable secondary binding agent.

The invention provides a substantially pure tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of the sequence set forth as SEQ ID NO:2, or a functional fragment of the tumor suppressor molecule. The invention also provides a substantially pure tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of the sequence set forth as SEQ ID NO:4, or a functional fragment of the tumor suppressor molecule.

As disclosed herein, SEQ ID NO:2, 5'-AGGGNGTCGGGGAGGT-3', represents a 16-nucleotide ribozyme binding sequence of an mRNA whose cleavage by a hairpin ribozyme having the corresponding substrate binding sequence 5'-ACCTCCCCAGAACCCT-3' (SEQ ID NO:1) resulted in unregulated cell proliferation (see Example II, below). SEQ ID NO:4, 5'-TAGTNGTCTACACTCT-3', represents a 16-nucleotide ribozyme binding sequence of an mRNA whose cleavage by a hairpin ribozyme having the corresponding substrate binding sequence

5'-AGAGTGTAAGAAACTA-3' (SEQ ID NO:3) resulted in unregulated cell proliferation (see Example II, below).

Fifteen contiguous nucleotides of a ribozyme binding sequence are sufficient for specific binding and effective cleavage by the corresponding hairpin ribozyme. Therefore, a tumor suppressor nucleic acid molecule of the invention contains at least fifteen contiguous nucleotides of the sequence set forth as SEQ ID NO:2 or SEQ ID NO:4. An exemplary tumor suppressor nucleic acid molecule that contains at least fifteen contiguous nucleotides of the sequence set forth as SEQ ID NO:2 is a nucleic acid molecule containing the nucleotide sequence set forth as SEQ ID NO:18, such as a nucleic acid molecule containing the nucleotide sequence set forth as SEQ ID NO:5.

A tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2, or a functional fragment thereof, does not consist of a nucleotide sequence having the exact endpoints of nucleotide sequences deposited in public databases at the time of filing, such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites (STSs) and genomic fragments, deposited in databases such as the nr, dbest, dbsts, gss and htgs databases, which are available for searching at http://www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=0, using the program BLASTN 2.0.9 [May-07-1999] described by Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997).

For example, a tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2, or a functional fragment thereof, does not consist of a nucleotide sequence having

the exact endpoints of sequences having the following Accession numbers: AC006022, Z54280, AC005739, X68128, AB014571, Z98755, AF030453, AC003104, AA406194, R12420, AI247609, AA278399, AI359294, AA495929, W84833, W84786, AA583557, T92983, AI078456, AI147476, H28699, AB016161, AB016160, D46041, D42474, C73064, AI084732, D24303, AA300789, AI147481, L00634, L10413, D29973, S69381, Z82189, AC005165, AA408534, AU017817, AI326830, AA655540, AA66686, AA211219, AA571392, AA160809, AU014594, AA511830, AA474138, C85533, AA408064, C87343, AA070605, AC003957, U09941, AC003695, AC002091, X64080, X98523, AJ011930, AC005668, U94776, D26094, Y00057, M15395, AA158729, AA357439, AA600873 and W87345.

Likewise, a tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:4, or a functional fragment thereof, does not consist of a nucleotide sequence having the exact endpoints of nucleotide sequences deposited in public databases at the time of filing, such as the databases described above, including sequences having the following Accession numbers: AB000909, AF067845 and AA492602.

A tumor suppressor nucleic acid molecule of the invention containing at least fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4 can be advantageously used, for example, as a detectable agent in the diagnostic methods of the invention, or to identify and isolate full-length tumor suppressor nucleic acid molecules by the methods disclosed herein. When used for such purposes, the nucleic acid molecule can contain none, one, or many nucleotides at the 5' or 3' end, or both, of the fifteen contiguous nucleotides. These additional nucleotides can correspond to the native

sequence of the tumor suppressor nucleic acid molecule, or can be non-native sequences, or both. For example, non-native flanking sequences that correspond to a restriction endonuclease site or a tag, or which stabilize the 15-nucleotide sequence in a hybridization assay, can be advantageous when the nucleic acid molecule is used as a probe or primer to identify or isolate longer tumor suppressor nucleic acid molecules.

A tumor suppressor nucleic acid molecule of the invention containing at least fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4, and additional sequence corresponding to a tumor suppressor nucleic acid molecule, can be used, for example, in the diagnostic and therapeutic methods disclosed herein. Native tumor suppressor nucleotide sequences flanking the fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4 can be determined by methods known in the art, such as RT-PCR, 5' or 3' RACE, screening of cDNA or genomic libraries, and the like, using an oligonucleotide having fifteen contiguous nucleotides of SEQ ID NO:2 of SEQ ID NO:4 as a primer or probe, and sequencing the resultant product (see Example III, below). The appropriate source of template RNA or DNA for amplification, extension or hybridization screening can be determined by those skilled in the art.

A specific example of a substantially pure tumor suppressor nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2 and flanking coding sequence is the tumor suppressor nucleic acid molecule having the nucleotide sequence set forth as SEQ ID NO:5. The isolation of SEQ ID NO:5, based on knowledge of the sequence of SEQ ID NO:2, is described in Example III, below. Similar procedures can be used to

identify and substantially purify longer nucleic acid molecules that contain at least fifteen contiguous nucleotides of SEQ ID NO:4. Such molecules and their functional fragments can be used to produce tumor suppressor polypeptides and specific antibodies, by methods known in the art and described herein, for use in the diagnostic and therapeutic methods described below.

As described previously, a tumor suppressor nucleic acid molecule, when functionally inactivated in a cell, causes the cell to proliferate in an unregulated manner. The tumor suppressor activity of a nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4 and additional native nucleic acid sequences can be further demonstrated using various methods known in the art and described herein. For example, nucleic acid sequences flanking the SEQ ID NO:2 or SEQ ID NO:4 sequences can be selectively targeted in a cell with ribozymes by the methods described in Example V, below. The effect on cell proliferation can be determined by the assays described below. If inactivation by ribozymal cleavage of a second sequence within the isolated nucleic acid molecule also results in unregulated cell proliferation, that nucleic acid molecule is a confirmed tumor suppressor nucleic acid molecule.

Similarly, other types of methods can be used to identify the tumor suppressor activity of a nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4. For example, an antibody or other selective agent that binds a polypeptide encoded by the nucleic acid molecule can be introduced into the cell, and the effect of the antibody on cell proliferation determined. Similarly, an

antisense oligonucleotide that inhibits transcription or translation of the nucleic acid molecule can be introduced into the cell, and the effect of the oligonucleotide on cell proliferation determined. Likewise, the candidate tumor suppressor nucleic acid molecule can be expressed in a cell. An introduced tumor suppressor nucleic acid molecule or its encoded polypeptide will have tumor suppressor activity, and thus inhibit cell proliferation or unregulated cell proliferatiaon. Those skilled in the art can determine other appropriate assays to demonstrate that a substantially pure nucleic acid molecule containing at least fifteen contiguous nucleotides of SEQ ID NO:2 or SEQ ID NO:4 has tumor suppressor activity.

The invention also provides a substantially pure nucleic acid molecule containing substantially the same nucleotide sequence as SEQ ID NO:5, or a functional fragment thereof. The invention further provides a substantially pure nucleic acid molecule encoding substantially the same amino acid sequence as SEQ ID NO:6, or encoding a functional fragment thereof.

SEQ ID NO:5 is a tumor suppressor nucleic acid molecule designated Human Tumor Suppressor-1, or HTS1. The nucleotide sequence of HTS1 is shown in Figure 6A, and its encoded amino acid sequence (SEQ ID NO:6) is shown in Figure 6B. Reducing HTS1 mRNA expression in HF cells, using a variety of ribozymes that target HTS1, promotes soft agar colony formation (see Examples II, IV and V, below). Introduction of HTS1 into Hela cells prevents cell proliferation (see Example VI, below).

Thus, a substantially pure nucleic acid molecule containing substantially the same nucleotide sequence as SEQ ID NO:5, or a functional fragment thereof, and a substantially pure nucleic acid molecule encoding substantially the same amino acid sequence as SEQ ID NO:6, or encoding a functional fragment thereof, are tumor suppressor nucleic acid molecules that can be used in the diagnostic and therapeutic methods disclosed herein.

The HTS1 nucleotide sequence (SEQ ID NO:5) disclosed herein has from 96% to 100% identity over portions of its sequence ranging from 98 nucleotides to 447 nucleotides, as determined by BLAST analysis, with human sequences present in the GenBank database having the following Accession numbers: AI084732; AA909530; AI061239; AI147481; AI000807; AA600054; AA281492; AA969975; N34073; AA321112; AI278754; AA989727; AA989727; AA321111; AI285506; AI285506; T16079; AI468710; AA258103; AA310412; AA300789; N40373; AA642297; AA622203; and AA622784. HTS1 (SEQ ID NO:5) also has from 83% to 88% identity over portions of its sequence ranging from 52 nucleotides to 508 nucleotides, as determined by BLAST analysis, with murine sequences present in the GenBank database having the following Accession numbers: AA561626; AA265569; AA237717; AA756790; AA270523; AA517621; W14218; AI325663; AA028364; AA451276; AA068339; W70806; AA475332; AA575760; AA238210; AA239726; AA638785; AA867627; and AI117891. HTS1 (SEQ ID NO:5) also has from 93% identity over a 32 nucleotide portion of its sequence with Dictyostelium discoideum sequences having GenBank Accession numbers AU036921 and C91439, and further has 100% identity over a 21 nucleotide portion of its sequence with Oryctolagus cuniculus sequences having GenBank Accession numbers C82711 and C83567.

A substantially pure nucleic acid molecule containing substantially the same nucleic acid sequence as SEQ ID NO:5, or a functional fragment thereof, does not consist of a nucleotide sequence having the exact endpoints of nucleotide sequences deposited in public databases at the time of filing, such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites (STSs) and genomic fragments, deposited in databases such as the nr, dbest, dbsts, gss and htgs databases, including sequences having the Accession numbers recited above.

A substantially pure nucleic acid molecule containing substantially the same nucleotide sequence as SEQ ID NO:5, or a functional fragment thereof, will be of sufficient length and identity to SEQ ID NO:5 to selectively hybridize to it under moderately stringent hybridization conditions. For example, it can be determined that a substantially pure nucleic acid molecule contains substantially the same nucleotide sequence as SEQ ID NO:5, or is a functional fragment thereof, by determining its ability to hybridize in a filter hybridization assay to a molecule having the sequence of SEQ ID NO:5, but not to other unrelated nucleic acid molecules, under moderately stringent hybridization conditions equivalent to hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2X SSPE, 0.2% SDS, at 65°C. Suitable alternative buffers and hybridization conditions that provide for moderately stringent hybridization conditions in particular assay formats can be determined by those skilled in the art (see, for example, Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989).

The invention further provides a substantially pure hairpin ribozyme nucleic acid molecule, containing a nucleotide sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:3. The hairpin ribozymes of the invention selectively bind, through the substrate binding sequences SEQ ID NO:1 and SEQ ID NO:3, to tumor suppressor mRNA molecules having the ribozyme binding sequences SEQ ID NO:2 and SEQ ID NO:4, respectively. For example, a hairpin ribozyme having the substrate binding sequence of SEQ ID NO:1 binds the HTS1 nucleotide sequence designated SEQ ID NO:18.

A substantially pure hairpin ribozyme of the invention can be catalytic, so as to bind and cleave a tumor suppressor nucleic acid messenger RNA. A catalytic hairpin ribozyme of the invention can therefore be used to selectively regulate the activity of a tumor suppressor nucleic acid molecule of the invention. A substantially pure hairpin ribozyme of the invention can also be catalytically disabled, for example, by replacement of the Loop 2 AAA sequence indicated in Figure 1 with a UGC sequence, so as to bind, but not cleave, a tumor suppressor nucleic acid molecule of the invention. A non-catalytic hairpin ribozyme can be used, for example, as a control reagent, or as a hybridization probe to identify tumor suppressor nucleic acid molecules in the diagnostic methods described herein.

The nucleic acid molecules of the invention, including tumor suppressor nucleic acid molecules and fragments, and hairpin ribozyme nucleic acid molecules, can be produced or isolated by methods known in the art. The method chosen will depend, for example, on the type of nucleic acid molecule one intends to isolate. Those skilled in the art, based on knowledge of the nucleotide

sequences disclosed herein, can readily isolate tumor suppressor nucleic acid molecules as genomic DNA, or desired introns, exons or regulatory sequences therefrom; as full-length cDNA or desired fragments therefrom; or as full-length mRNA or desired fragments therefrom, by methods known in the art. Likewise, those skilled in the art can produce or isolate hairpin ribozymes selective for these sequences.

A useful method of isolating a tumor suppressor nucleic acid molecule of the invention involves amplification of the nucleic acid molecule using the polymerase chain reaction (PCR), and purification of the resulting product by gel electrophoresis. For example, either PCR or reverse-transcription PCR (RT-PCR) can be used to produce a tumor suppressor nucleic acid molecule having any desired nucleotide boundaries. Desired modifications to the nucleic acid sequence can also be introduced by choosing an appropriate primer with one or more additions, deletions or substitutions. Such nucleic acid molecules can be amplified exponentially starting from as little as a single gene or mRNA copy, from any cell, tissue or species of interest.

A futher method of producing or isolating a tumor suppressor nucleic acid molecule of the invention is by screening a library, such as a genomic library, cDNA library or expression library, with a detectable agent. Such libraries are commercially available or can be produced from any desired tissue, cell, or species of interest using methods known in the art. For example, a cDNA or genomic library can be screened by hybridization with a detectably labeled nucleic acid molecule having a nucleotide sequence disclosed herein. Additionally, an expression library can be screened with an antibody

raised against a polypeptide corresponding to the coding sequence of a tumor suppressor nucleic acid disclosed herein. The library clones containing tumor suppressor nucleic acid molecules of the invention can be purified away from other clones by methods known in the art.

Furthermore, nucleic acid molecules of the invention can be produced by sythetic means. For example, a single strand of a nucleic acid molecule can be chemically synthesized in one piece, or in several pieces, by automated synthesis methods known in the art. The complementary strand can likewise be synthesized in one or more pieces, and a double-stranded molecule made by annealing the complementary strands. Direct synthesis is particularly advantageous for producing relatively short molecules, such as hairpin ribozyme nucleic acid molecules, as well as hybridization probes and primers.

If it is desired to subclone, amplify or express a substantially pure nucleic acid molecule of the invention, the isolated nucleic acid molecule can be inserted into a commercially available cloning or expression vector using methods known in the art. Appropriate regulatory elements can be chosen, if desired, to provide for constitutive, inducible or cell type-specific expression in a host cell of choice, such as a bacterial, yeast, amphibian, insect or mammalian cell. Those skilled in the art can determine an appropriate host and vector system for cloning a nucleic acid molecule of the invention or for expressing and purifying its encoded polypeptide.

Methods for introducing a cloning or expression vector into a host cell are well known in the art and include, for example, various methods of

transfection such as the calcium phosphate, DEAE-dextran and lipofection methods, viral transduction, electroporation and microinjection. Host cells expressing tumor suppressor nucleic acid molecules can be used, for example, as a source to isolate recombinantly expressed tumor suppressor polypeptides, to identify and isolate molecules that regulate or interact with tumor suppressor nucleic acids and polypeptides, or to screen for compounds that enhance or inhibit the activity of a tumor suppressor molecule of the invention, as described further below.

The methods of isolating, cloning and expressing nucleic acid molecules of the invention described herein are routine in the art and are described in detail, for example, in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1992) and in Ansubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, MD (1989), which are incorporated herein by reference.

The invention also provides a substantially pure polypeptide, containing substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof. SEQ ID NO:6 is a full-length tumor suppressor polypeptide molecule designated Human Tumor Suppressor-1, or HTS1, which is encoded by SEQ ID NO:5.

The HTS1 amino acid sequence disclosed herein (SEQ ID NO:6) has 36% identity over a 402 amino acid portion, as determined by BLAST analysis, with a *Drosophila melanogaster* polypeptide designated Peter Pan, having GenBank Accession number AAD16459 (AF102805); 36% identity over 340 amino acids with a Caenorhabditis

elegans polypeptide having GenBank Accession number 2804465 (AF043700); 37% identity over 289 amino acids with a Schizosaccharomyces pombe polypeptide having GenBank Accession number CAB11063 (Z98531); and 35% identity over 345 amino acids with Saccharomyces cervisiae polypeptides having GenBank Accession numbers Q12153 and P38789.

A substantially pure polypeptide containing substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof, does not consist of an amino acid sequence having the exact endpoints of amino acid sequences deposited in public databases at the time of filing the application, such as GenBank, EMBL, SwissProt and similar databases, including sequences having the Accession numbers recited above.

Furthermore, a substantially pure polypeptide containing substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof, does not consist of the 137 amino acid *Homo sapiens* polypeptide sequence depicted in Figure 4 of Migeon et al., Mol. Biol. Cell. 10:1733-1744 (1999) (see Figure 7, "HS," also SEQ ID NO:20), deduced from compilation of expressed sequence tag fragments N34073, N40373, AI147481, AI084732, AA321112, AA300789 and AA258103. Additionally, a substantially pure polypeptide containing substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof, does not consist of the 358 amino acid *Mus musculus* polypeptide sequence depicted in Figure 4 of Migeon et al., supra (1999) (see Figure 7, "MM," also SEQ ID NO:19), deduced from compilation of expressed sequence tag fragments AA451276, AA475332, AA068339, AA237717, AA517621, AA270523, AA756790, AA028364, AA575760, AA239726, AA561626, and AA265569.

The isolated tumor suppressor polypeptides and functional fragments of the invention can be prepared by methods known in the art, including biochemical, recombinant and synthetic methods. For example, a tumor suppressor polypeptide can be purified by routine biochemical methods from a cell or tissue source that expresses abundant amounts of the corresponding transcript or polypeptide. The diagnostic methods disclosed herein can be adapted for determining which cells and tissues, and which subcellular fractions therefrom, are appropriate starting materials. Biochemical purification can include, for example, steps such as solubilization of the appropriate tissue or cells, isolation of desired subcellular fractions, size or affinity chromatography, electrophoresis, and immunoaffinity procedures. The methods and conditions for biochemical purification of a polypeptide of the invention can be chosen by those skilled in the art, and purification monitored, for example, by an ELISA assay or a functional assay.

A fragment having any desired boundaries and modifications to the tumor suppressor amino acid sequences disclosed herein can also be produced by recombinant methods. Recombinant methods involve expressing a nucleic acid molecule encoding the desired polypeptide or fragment in a host cell or cell extract, and isolating the recombinant polypeptide or fragment, such as by routine biochemical purification methods described above. To facilitate identification and purification of the recombinant polypeptide, it is often desirable to insert or add, in-frame with the coding sequence, nucleic acid sequences that encode epitope tags, polyhistidine tags, glutathione-S-transferase (GST) domains, and similar affinity binding sequences, or

sequences that direct expression of the polypeptide in the periplasm or direct secretion. Methods for producing and expressing recombinant polypeptides *in vitro* and in prokaryotic and eukaryotic host cells are well known in the art.

Functional fragments of a tumor suppressor polypeptide can also be produced, for example, by enzymatic or chemical cleavage of the full-length polypeptide. Methods for enzymatic and chemical cleavage and for purification of the resultant peptide fragments are well known in the art (see, for example, Deutscher, Methods in Enzymology, Vol. 182, "Guide to Protein Purification," San Diego: Academic Press, Inc. (1990), which is incorporated herein by reference).

Furthermore, functional fragments of a tumor suppressor polypeptide can be produced by chemical synthesis. If desired, such as to optimize their functional activity, stability or bioavailability, such molecules can be modified to include D-stereoisomers, non-naturally occurring amino acids, and amino acid analogs and mimetics. Examples of modified amino acids and their uses are presented in Sawyer, Peptide Based Drug Design, ACS, Washington (1995) and Gross and Meienhofer, The Peptides: Analysis, Synthesis, Biology, Academic Press, Inc., New York (1983), both of which are incorporated herein by reference.

As described previously, a substantially pure polypeptide containing substantially the same amino acid sequence as SEQ ID NO:6, or a functional fragment thereof, has one or more of the functional activities of HTS1 (SEQ ID NO:6). A functional activity can be, for example, immunogenicity, which is an ability to generate

an antibody specific for HTS1, or antigenicity, which is an ability to selectively compete with HTS1 for binding to an HTS-1-specific antibody.

Those skilled in the art can determine, by known methods, whether a particular polypeptide or fragment has the immunogenic or antigenic activity of HTS1. For example, to determine whether a polypeptide or fragment has immunogenic activity, the test polypeptide or fragment can be assayed to determine whether it induces a delayed-type hypersensitivity response in an animal sensitized to HTS1. Immunogenic activity can also be determined by elicitation of HTS-1-specific antibodies, as measured by an ELISA assay with HTS1. To determine whether a particular polypeptide or fragment has the antigenic activity of HTS1 and, thus, competes with HTS1 for binding to HTS-1-specific antibodies, various ELISA-type assays, including competitive ELISA, can be performed. Assays that can be used for determining HTS-1-specific immunogenic or antigenic activity of the polypeptides and fragments of the invention are described in more detail in Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1989), which is incorporated herein by reference.

If desired, random fragments spanning an entire HTS1 polypeptide sequence can be tested in the assays described above. Alternatively, only those fragments of HTS1 that are likely to be immunogenic or antigenic can be tested. Determination of whether a particular fragment is likely to be immunogenic or antigenic can be based on methods and algorithms known in the art and described, for example, by Margaht et al., J. Immunol. 138:2213-2229 (1987) and by Rothbard et al., EMBO J.

7:93-100 (1988), which are incorporated herein by reference.

A functional activity of an HTS1 polypeptide or fragment of the invention can also be its ability to alter, such as inhibit or promote, cell proliferation when expressed or introduced in a cell. To determine whether a given polypeptide or fragment has the ability to alter cell proliferation, the polypeptide or fragment can be microinjected into a cell, and an increase or decrease in cell proliferation determined by any of the proliferative assays described below. Alternatively, a polypeptide or fragment can be expressed in the cell by recombinant methods known in the art and as described previously.

Those skilled in the art appreciate that an HTS1 polypeptide that is substantially the same as a full-length native HTS1 tumor suppressor molecule, or that includes an entire tumor suppressing domain therefrom, will likely inhibit cell proliferation upon expression or introduction into a cell. However, a fragment or modification of a tumor suppressor polypeptide that possesses less than an entire tumor suppressing domain, or in which the tumor suppressing activity is inactivated, can compete with the endogenous or recombinantly expressed protein for substrates or regulatory factors. In this case, the modified polypeptide or functional fragment will inhibit the tumor suppressor activity of the endogenous or recombinantly expressed tumor suppressor polypeptide, thereby promoting cell proliferation.

Appropriate assays to determine whether a molecule of the invention alters cell proliferation are known in the art. The skilled artisan appreciates that molecular pathways involved in cell proliferation are generally well conserved among eukaryotic organisms. Therefore, a proliferative assay can be performed in any eukaryotic cell type in which altered proliferation can be detected including, for example, primary mammalian cells, normal and transformed mammalian cell lines, yeast, insect cells and amphibian cells.

A molecule that alters cell proliferation can, for example, cause cell cycle arrest at a particular stage of mitosis or meiosis, induce or prevent apoptosis, or promote progression through the cell cycle when normal cells would arrest. Such qualitative changes in the cell cycle can be determined by methods known in the art, and which depend on the cell type used in the assay. A molecule that alters cell proliferation can also, for example, cause faster or slower progression through the cell cycle, resulting in an increased or decreased number of cells in the population after a given period of time. Those skilled in the art can choose an appropriate assay to determine whether and how a molecule of the invention affects cell proliferation.

A molecule that alters cell proliferation can also restore more normal proliferative characteristics on an abnormally proliferating cell. Such a molecule can advantageously be used in therapeutic applications to treat proliferative disorders. To determine whether a molecule of the invention restores more normal proliferative characteristics on a cell, an assay can be performed in a mammalian cell that exhibits neoplastic proliferative characteristics, such as soft agar colony

formation, overgrowth of a cell monolayer, proliferation in low serum, abnormally rapid proliferation, or tumor formation in an animal. Such cells are known in the art and include both tumor cell lines and primary tumor cells. A molecule of the invention can be introduced or expressed in such a cell, and a determination can be made whether the molecule restores more normal proliferative characteristics to the cell, such as slower growth in culture, fewer foci, fewer soft agar colonies, or a reduction in tumor size, as compared to the parental cell.

An HTS1 tumor suppressor molecule that restores normal proliferative characteristics to a neoplastic cell in an assay described above can be administered to an individual, such as a human or other mammal, so as to be introduced or expressed in the neoplastic cell in an amount effective to prevent or inhibit its unregulated proliferation. For example, a nucleic acid molecule encoding a polypeptide that inhibits cell proliferation can be inserted into a mammalian expression vector, such as a plasmid or viral vector, that contains all the necessary expression elements for the constitutive or inducible transcription and translation of the polypeptide, and administered to an individual having, or at risk of developing a tumor.

Useful mammalian expression vectors for gene therapy, and methods of introducing such vectors into cells, are well known in the art. For example, a plasmid expression vector can be introduced into a cell by calcium-phosphate mediated transfection, DEAE-Dextran-mediated transfection, lipofection, polybrene-mediated transfection, electroporation or any other method known in the art of introducing DNA into a

cell. A viral expression vector can be introduced into a cell in an expressible form by infection or transduction, for example, or by encapsulation in a liposome. An appropriate viral vector for gene therapy applications can be, for example, a retrovirus, an adenovirus, an adeno-associated virus or a herpes virus.

A physiological composition, such as an aqueous solution, suspension or emulsion, containing an effective concentration of an expressible nucleic acid can be administered by any effective route, such as topically, intraocularly, intradermally, parenterally, orally, intranasally, intravenously, intramuscularly, intraspinally, intracerebrally and subcutaneously. For example, the physiological composition can be directly injected into a solid tumor, tumor-containing organ or tumor containing body cavity, in a effective amount to inhibit proliferation of the tumor cells. Alternatively, the physiological composition can be administered systemically into the blood or lymphatic circulation to reach tumor cells in the circulatory system or in any organ or tissue. Therefore, the tumor suppressor molecules of the invention can be used to treat both solid tumors (carcinomas and sarcomas) and leukemias.

An effective dose of a therapeutic molecule of the invention can be determined, for example, by extrapolation from the concentration required to modulate tumor suppressor nucleic acid or polypeptide expression in the expression assays described herein, or from the dose required to modulate cell proliferation in the proliferation assays described herein.

An effective dose of a molecule of the invention for the treatment of proliferative disorders can also be determined from appropriate animal models, such as xenografts of human tumors in rats or mice. Human cancer cells can be introduced into an animal by a number of routes, including subcutaneously, intraveneously and intraperitoneally. Following establishment of a tumor, the animals can be treated with different doses of a molecule of the invention, and tumor mass or volume can be determined. An effective dose for treating cancer is a dose that results in either partial or complete regression of the tumor, reduction in metastasis, reduced discomfort, or prolonged lifespan.

The appropriate dose for treatment of a human subject with a therapeutic molecule of the invention can be determined by those skilled in the art, and is dependent on the nature and bioactivity of the particular compound, the desired route of administration, the gender, age and health of the individual, the number of doses and duration of treatment, and the particular condition being treated.

The invention also provides an antibody or antigen binding fragment thereof specifically reactive with an HTS1 tumor suppressor polypeptide or functional fragment of the invention. Such antibodies can be used, for example, to affinity purify an HTS1 polypeptide from a cell or tissue source. Such antibodies can also be used to detect the expression of the polypeptide in a sample, or to selectively detect an abnormal structural variant of the polypeptide, in the diagnostic methods described herein. An antibody can be labeled with a detectable moiety so as to render it detectable by analytical methods. For example, a detectable moiety can

be directly or indirectly attached to the antibody. Useful detectable moieties include, for example, enzymes, fluorogens, chromogens, chemiluminescent labels and secondary binding agents.

Antibodies that selectively detect an abnormal structural variant of HTS1 can also be administered therapeutically, to selectively target cells that express the altered copy of the polypeptide. If desired, such antibodies can be administered in conjuction with a cytotoxic or cytostatic moiety, such as a radioisotope or toxin, in order to neutralize or kill cells expressing the abnormal structural variant.

An antigen binding fragment of an antibody of the invention includes, for example, individual heavy or light chains and fragments thereof, such as VL, VH and Fd; monovalent fragments, such as Fv, Fab, and Fab'; bivalent fragments such as $F(ab')_2$; single chain Fv (scFv); and Fc fragments. Antigen binding fragments include, for example, fragments produced by protease digestion or reduction of an antibody, as well as fragments produced by recombinant DNA methods known to those skilled in the art.

The antibodies of the invention can be produced by any method known in the art, and can be polyclonal or monoclonal. For example, a polypeptide or immunogenic fragment of the invention, or a nucleic acid expressing such a polypeptide, can be administered to an animal, using standard methods, and the antibodies isolated therefrom. The antibodies can be used in the form of serum isolated from an immunized animal or the antibody can be purified from the serum. Additionally, the antibodies can be produced by a hybridoma cell line, by

chemical synthesis, or by recombinant methods. Modified antibodies, such as chimeric antibodies, humanized antibodies and CDR-grafted or bifunctional antibodies, can also be produced by methods well known to those skilled in the art.

Methods of preparing and using antibodies and antigen-binding fragments, including detectably labeled antibodies, are described, for example, in Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (1989); in Day, E.D., Advanced Immunochemistry, Second Ed., Wiley-Liss, Inc., New York, NY (1990); and in Borrebaeck (Ed.), Antibody Engineering, Second Ed., Oxford University Press, New York (1995), which are incorporated herein by reference.

As described herein, functional inactivation of a tumor suppressor molecule of the invention by cleavage of the mRNA with a hairpin ribozymes promotes unregulated, neoplastic proliferation. Therefore, by detecting functional inactivation of a tumor suppressor molecule in a sample, one can detect the presence of a neoplastic cell in the sample. In an individual with a neoplasia, inactivation of the tumor suppressor nucleic acid molecule could have occurred by any of a variety of different mutational mechanisms including, for example, frameshift mutations, nonsense mutations, deletions and rearrangements, which alter the expression or structure, and thus affect the normal function, of the tumor suppressor molecule. In different neoplastic cell types, and at different stages in tumor development, it is expected that different mutational events will have occurred.

The invention thus provides a method of detecting a neoplastic cell in a sample. In one embodiment, the method consists of contacting the sample with a detectable agent specific for a tumor suppressor nucleic acid molecule of the invention, and detecting the nucleic acid molecule in the sample. Altered expression or structure of the nucleic acid molecule indicates the presence of a neoplastic cell in the sample. In another embodiment, the method consists of contacting the sample with a detectable agent specific for a tumor suppressor polypeptide of the invention, and detecting the polypeptide in the sample. Altered expression or structure of the polypeptide indicates the presence of a neoplastic cell in the sample.

The diagnostic methods described herein are applicable to the identification of neoplastic cells present in solid tumors (carcinomas and sarcomas) such as, for example, breast, colorectal, gynecological, lung, prostate, bladder, renal, liver, urethral, endocrinal, melanoma, basal cell, central nervous system, lymphoma, stomach, esophageal, squamous cell cancers, as well as all forms of leukemia and lymphoma.

Various qualitative and quantitative assays to detect altered expression or structure of a nucleic acid molecule in a sample are well known in the art, and generally involve hybridization of a detectable agent, such as a complementary primer or probe, to the nucleic acid molecule. Such assays include, for example, *in situ* hybridization, which can be used to detect altered chromosomal location of the nucleic acid molecule, altered gene copy number, or altered RNA abundance, depending on the format used. Other assays include, for example, Northern blots and RNase protection assays,

which can be used to determine the abundance and integrity of RNA; Southern blots, which can be used to determine the copy number and integrity of DNA; SSCP analysis, which can detect single point mutations in DNA, such as in a PCR or RT-PCR product; and coupled PCR, transcription and translation assays, such as the Protein Truncation Test, in which a mutation in DNA is determined by an altered protein product on an electrophoresis gel. An appropriate assay format and detectable agent to detect an alteration in the expression or structure of a tumor suppressor nucleic acid molecule can be determined by one skilled in the art depending on the alteration one wishes to identify.

Various assays to detect altered expression or structure of a polypeptide of the invention are also well known in the art, and generally involve hybridization of a detectable agent, such as an antibody or selective binding agent, to the polypeptide in a sample. Such assays can be performed *in situ*, such as by immunohistochemistry or immunofluorescence, in which a detectably labeled antibody contacts a polypeptide in a cell. Other assays, for example, ELISA assays, immunoprecipitation, and immunoblot analysis, can be performed with cell or tissue extracts. Assays in which the polypeptide remains in a native form are particularly useful if a conformation-specific binding agent is used, which can detect a polypeptide with an altered structure. A structural variant of a tumor suppressor polypeptide can act, for example, in a dominant-negative fashion to inactivate a normal regulatory pathway and cause unregulated cell proliferation. An appropriate assay format and detectable agent to detect an alteration in the expression or structure of a tumor suppressor

polypeptide can be determined by one skilled in the art depending on the alteration one wishes to identify.

The diagnostic methods described herein can also be adapted for use as prognostic assays. Such an application takes advantage of the observation that alterations in expression or structure of different tumor suppressor molecules take place at characteristic stages in the progression of a proliferative disease or of a tumor. Knowledge of the stage of the tumor allows the clinician to select the most appropriate treatment for the tumor and to predict the likelihood of success of that treatment. The diagnostic methods described herein can also be used to monitor the effectiveness of therapy. Successful therapy can be indicated, for example, by a reduction in the number of neoplastic cells in an individual, as evidenced by more normal expression and structure of the tumor suppressor molecules of the invention in a sample following treatment.

In the diagnostic and prognostic assays described herein, the abundance or structure of the detected nucleic acid or polypeptide in the test sample is compared to the known abundance or structure of the nucleic acid or polypeptide in a normal sample. The normal sample can be obtained either from normal tissue of the same histological origin of the same or a different individual.

The invention further provides a method of identifying cellular and non-cellular molecules that selectively bind, mimic or regulate the tumor suppressor molecules of the invention. Various binding assays to identify cellular proteins that interact with protein binding domains are known in the art and include, for

example, yeast two-hybrid screening assays (see, for example, Luban et al., Curr. Opin. Biotechnol. 6:59-64 (1995)) and affinity column chromatography methods using cellular extracts. Additionally, binding compounds can be identified by screening libraries of compounds, including chemical or biological molecules such as simple or complex organic molecules, metal-containing compounds, carbohydrates, peptides, proteins, peptidomimetics, glycoproteins, lipoproteins, nucleic acids, antibodies, and the like, using methods known in the art.

Compounds that selectively bind to tumor suppressor molecules can be used, for example, to detect the presence, abundance or structural integrity of tumor suppressor molecules in the diagnostic methods described herein. Compounds that mimic or activate the tumor suppressor molecules of the invention in cell-based assays can be used, for example, as therapeutics to treat proliferative disorders such as cancer, either alone or when attached to a cytotoxic or cytostatic agent. The proliferative assays described herein can be used to identify compounds that mimic or activate tumor suppressor biological activity and are thus appropriate therapeutic compounds to treat cancer.

It is understood that modifications which do not substantially affect the activity of the various embodiments of this invention are also included within the definition of the invention provided herein. Accordingly, the following examples are intended to illustrate but not limit the present invention.

EXAMPLE I

Preparation of the random retroviral vector ribozyme library

This example demonstrates the construction of a random retroviral plasmid ribozyme gene library. The inventors have discovered that by introducing a random retroviral plasmid ribozyme gene library into the Hela cell revertant cell line, HF, certain of the ribozymes will selectively target and inactivate mRNA molecules encoding tumor suppressor genes. If the ribozyme has inactivated a tumor suppressor nucleic acid molecule, the HF cells will proliferate in an unregulated fashion and form soft agar colonies. The ribozyme genes are then rescued from these soft agar colonies and sequenced across their substrate binding sites. The corresponding ribozyme binding sequence, or "ribozyme sequence tag" (RST) is a sequence present in the tumor suppressor nucleic acid molecule targeted by the ribozyme. Thus, knowledge of the RST allows novel tumor suppressor nucleic acids to be identified and isolated.

A plasmid-based retroviral library was constructed by inserting random ribozyme gene sequences into parent vector pLHPM-2kb. pLHPM-2kb contains 5' and 3' long terminal repeats (LTR) of the Moloney retroviral genome; a neomycin resistance gene driven by the LTR; an SV40 promoter driving a puromycin resistance gene; and a transcription cassette containing a tRNAval promoter and a 2 kb stuffer insert. When the stuffer insert is removed and replaced by the random ribozyme library inserts, the tRNAval promoter can drive transcription of the inserted ribozyme gene.

To prepare the pLHPM-2kb vector, plasmid pLHPM was digested overnight at 65°C with BstB1, phenol:chloroform extracted and ethanol precipitated. The resuspended DNA was then digested overnight at 37°C with MluI. This double digestion excises the 2kb stuffer fragment. The resultant 6kb plasmid vector DNA fragment was purified by agarose gel electrophoresis.

To prepare the random ribozyme library inserts, three oligonucleotides were synthesized and annealed in annealing buffer (50 mM NaCl, 10 mM Tris pH 7.5, 5 mM MgCl2) at a molar ratio of 1:3:3 (oligo1:oligo2:oligo3) by heating to 90°C followed by slow cooling to room temperature. The three oligonucleotides had the following sequences:

Oligo1: 5'-pCGCGTACCAGGTAATATACCACGGACCGAAGTCCGTGTGTTTCT CTGGTNNNNTTCTNNNNNNNNGGATCCTGTTTCCGCCCGGTTT-3' (SEQ ID NO:7)

Oligo2: 5'-pGTCCGTGGTATATTACCTGGTA-3' (SEQ ID NO:8)

Oligo3: 5'-pCGAAACCGGGCGGAAACAGG-3' (SEQ ID NO:9)

To provide for random and uniform incorporation of A, T, C and G nucleotides at the positions represented as N nucleotides in oligo1, the A, T, C and G reagents were premixed, and the same mixture used for every N position in the oligonucleotide synthesis. The ribozyme insert library formed by annealing the three oligonucleotides (SEQ ID NOS:7-9) thus contains 8 positions with random nucleotides corresponding to helix 1 of the ribozyme, and 4 random positions with random nucleotides corresponding to helix 2 of the ribozyme.

In order to ligate the pLHPM-2kb vector DNA fragment with the random ribozyme insert library, 0.5 pmole of the vector and an 8-fold molar excess of annealed oligonucleotides were ligated overnight with 10 units of T4 DNA ligase. Ultracompetent DH12S bacteria were then electroporated with the ligation mixture. A total of 5 x 10^7 bacterial colonies containing the retroviral plasmid ribozyme library was obtained.

The bacterial colonies containing the retroviral plasmid ribozyme library were pooled in aliquots as a master stock and frozen at -80°C. Working stocks were made by culturing 1 ml of the master stock in 60 ml LB media overnight at 30°C. A 1 ml aliquot of the working stock was used to make a 500 ml bacterial culture by incubation at 30°C overnight. Plasmid DNA was then extracted from the 500 ml culture and transfected into HF revertant cells, as described in Example II, below.

Following the cloning of the randomized hairpin ribozyme genes into pLHPM, the "randomness" of the plasmid library was evaluated by both statistical and functional analyses. A complete ribozyme library of this design, with 12 random positions, would contain 412, or 1.67 x 10^7, different members. For the statistical analysis, forty individual bacterial transformants were picked and sequenced. This allowed an evaluation of the complexity of the library without having to manually sequence each library member. The statistical "randomness" of the library was determined utilizing the formula for a two- sided approximate binomial confidence interval: E= 1.96*squareroot(P*(1-P)/N), where P= the expected proportion of each nucleotide in a given position (this value for DNA bases equals 25% or P=O.25), E=the desired confidence interval around P (i.e. P+/-E)

and N=the required sample size (Callahan Associates, Inc., La Jolla, CA). To determine the proportion of each base within 5% (E=0.05), the required sample size is 289. Since each ribozyme molecule contains twelve independent positions, the number of individual ribozyme genes that need to be sequenced out of the library equals 289 divided by 12, or about 25 molecules.

The frequencies of the four nucleotides, with 95% confidence limits, in the random positions were calculated to be G: 22.3 $\pm$6.1, A: 3 1.9$\pm$7.0, T: 27.3$\pm$7.8 and C: 18.01$\pm$15.1. Since the expected frequency for each base is 25%, each base appears to be randomly represented (except for C, which may be slightly lower than expected). These variations most likely result from the unbalanced incorporation of nucleotides during the chemical synthesis of the oligonucleotides and could reduce the complexity of the library.

For a functional evaluation of the library's complexity, *in vitro* cleavage was utilized to determine if ribozymes that target known RNA substrates were present in the library pool. This involved *in vitro* transcribing of the entire ribozyme library in one reaction and then testing the pool's ability to cleave a variety of different RNA substrates of both cellular and viral origin. Six out of seven known RNA targets were properly and efficiently cleaved by the *in vitro* transcribed library. This qualitative analysis suggested a significantly complex library of ribozyme genes and the lack of cleavage of one target out of seven may reflect the slight non-randomness suggested by the base composition described above.

EXAMPLE II

Isolation of ribozymes that target tumor suppressor nucleic acids

This example demonstrates the isolation of ribozyme genes that bind to and inactivate tumor suppressor nucleic acid molecules, and the identification of the nucleic acid sequences they target.

The Hela revertant cell line, HF, used in these experiments was produced by exposure of Hela cervical carcinoma cells to the mutagen EMS, and subsequent isolation of a stable clone that had lost transforming properties. The HF cell line is described by Boylan et al., Cell Growth Differ. 7:725-735 (1996). In contrast to Hela cells, HF cells do not exhibit a transformed morphology and are non-tumorigenic in nude mice. HF cells are also anchorage dependent, as evidenced by a very low cloning efficiency in soft agar (0.05%), compared with 20% for the parental Hela cells. Boylan et al., supra (1996) observed that fusion of HF cells with Hela cells resulted in a loss of the transformed phenotype in the fusion cells. This observation indicated that the HF cells express one or more dominant tumor suppressor genes.

Both Hela and HF cells were cultured at 37°C in DMEM (Gibco BRL) supplemented with 10% FBS, L-gln, sodium pyruvate and antibiotics. For stable library delivery, 1 x 10^8 HF cells were transfected with the ribozyme plasmid library using the BES-calcium phosphate method. 24 hours post transfection, cells were selected with G418 (500 pg/ml) for two weeks. Approximately 1 x 10^7 stable transfectants were generated following G418 selection as

determined by colony formation, and all colonies were pooled prior to soft agar selection.

To determine whether any of the transfectants had regained their transformed phenotype, soft agar selection of the library was performed in forty 150 mm^2 plates, pre-layered with 12 ml of a 1:1 mixture of 1.2% Select Agar (GibcoBRL, Rockville, MD): 2X MEM/20% FBS. After the pre-layer had solidified, 3 x 10^5 cells were plated in the "cell layer" consisting of 12 ml of a 1:1 mixture of 0.6% Select Agar: 2X MEM/20% FBS. As a control, 1.2 x 10^6 HF cells stably transfected with an unrelated Rz, CNR3, were plated into four 150 mm^2 soft agar plates. As comparisons, 3 x 10^5 Hela or HF parental (untransfected) were plated into one 150 mm^2 plate each. The cell layers were allowed to solidify prior to incubation at 37°C. Soft agar plates were fed once per week by layering 8 ml freshly prepared 1:1 mixture of 0.6% Agar Select: 2X MEM/20% FBS. Colonies were visible by two weeks and picked for expansion and analysis at 3 weeks. Following three weeks in soft agar, colonies appeared in both the Rz library and CNR3 control Rz, however the library-expressing cells produced 2.5-fold more colonies than the control Rz and 4-fold more than untransfected HF cells (Table 1).

Table 1

Cells	**Primary Selection (colonies/10^5)**	**Secondary Selection (colonies/10^5)**
Hela	50,000	50,000
HF Parental	10	25
HF-Control Rz	20	48
HF-Rz Library	45	15,000

To determine whether the cells that grew as colonies in soft agar had a stable phenotype, 300 colonies from the library expressing cells, 100 colonies from the CNR3 HF-control, or 30 colonies from either Hela or HF parental were picked from the first round, pooled and expanded for 2 weeks in normal media. Second round soft agar selection was performed with 3 x 10^5 cells in one 150 mm^2 plate for each cell type. Both the HF parental and the HF^- control cells showed only modest (2- to 3-fold) enrichment in soft agar growth, indicating that colony growth in the controls was mostly due to unstable, stochastic processes. In contrast, the library-expressing cells showed a dramatic 300-fold increase, suggesting that ribozymes from the library stably enhanced soft agar growth (Table 1).

Two methods of ribozyme gene rescue were performed in parallel, viral rescue and PCR rescue, on the pool of 300 colonies from the first round of soft agar selection. The first method, viral rescue, takes advantage of the fact that the Rz expression cassette is located between packagable retroviral LTRs. Rz-expressing cells were transiently transfected with the retroviral gag, pol and VSV-G envelope genes using the lipid transfection reagent LT1 (available from Miris Laboratories, distributed by Panvera, Inc.). 6.3 µg each pEnv- (Moloney gag and pol) and pVSV-G (vesicular stomatitis virus G glycoprotein to serve as the retroviral envelope) per 100 mm^2 dish, according to the manufacturer's instructions. 24-48 hours later, viral supernatant was recovered and filtered (0.2 µm) prior to transduction of fresh HF cells in the presence of 4 µg/ml polybrene. Fresh HF cells were then transduced with the infectious supernatant, selected with G418 and plated into soft agar. Sequence analysis from the resulting

individual soft agar colonies revealed enrichment of one ribozyme, designated Rz 568, present in three out of ten clones.

The second method of Rz gene rescue was performed by PCR amplification of the genomic DNA from the selected pool of cells, followed by batch recloning of the Rz genes into the pLHPM vector. PCR rescue was performed on genomic DNA, isolated from the selected cells using the QIAamp Blood Kit (Qiagen, Valencia, CA). PCR primers within the vector amplified a 300 bp fragment containing the ribozyme genes. The PCR product, which contained a pool of Rz genes, was then digested with BamHI and MluI and ligated into pLHPM digested with the same enzymes. The resulting bacterial clones were pooled and purified DNA was used for cell transfections. Fresh HF cells were stably transfected and plated into soft agar. In this rescue, Rz 568 was present in five out of ten soft agar colonies.

Sequence results from the viral and PCR rescues suggested that Rz 568 was conferring a selective growth advantage to HF cells plated in soft agar. To verify this finding, the 568 ribozyme gene was stably transfected into fresh HF cells as described above. As a control, the catalytically disabled form of Rz 568 (d568, see Figure 1) was similarly cloned and transfected. After two rounds of selection, Rz 568, but not d568, significantly promoted HF soft agar growth (Figure 2), verifying that Rz 568 alone can confer this phenotype. Equally important, since d568 had no effect, it was concluded that the catalytic activity of Rz 568 is required for the phenotype, presumably by cleaving an mRNA involved in an anchorage-dependent growth pathway active in HF cells.

The substrate binding sequence of Rz 568, together with its corresponding ribozyme sequence tag (RST 568), is presented in Table 2, below.

Table 2

Rz 568 gene sequence	**Corresponding RST 568**
ACCTCCCC AGAA CCCT (SEQ ID NO:1)	AGGG NGTC GGGGAGGT (SEQ ID NO:2)

A second ribozyme gene was identified by the viral rescue procedure described above. Rz 619 has a stronger phenotype that Rz 568, ie. produces a higher number of soft agar colonies after transfection of HF cells. Expression of Rz 619 alters the morphology of HF cells to a transformed, highly refractile appearance. Rz 619 does not target the HTS1 mRNA, nor does it have any obvious database matches. The substrate binding sequence of this ribozyme (Rz 619), and its corresponding ribozyme sequence tag, designated RST 619, is presented in Table 3, below.

Table 3

Rz 619 gene sequence	**Corresponding RST 619**
AGAGTGTA AGAA ACTA (SEQ ID NO:3)	TAGT NGTC TACACTCT (SEQ ID NO:4)

In view of their ability to reproducibly cause a transformed phenotype when expressed in HF revertant cells, ribozymes containing substrate binding sequences designated SEQ ID NO:1 and SEQ ID NO:3 are ribozymes which target and inactivate tumor suppressor nucleic acid molecules. Likewise, the targets of these ribozymes, which are nucleic acid molecules containing nucleic acid

sequences designated SEQ ID NO:2 or SEQ ID NO:4, are tumor suppressor nucleic acid molecules.

EXAMPLE III

Isolation and characterization of Human Tumor Suppressor-1 (HTS1)

This example demonstrates the isolation of a full-length tumor suppressor nucleic acid molecule designated Human Tumor Suppressor-1 (HTS1) cDNA and its encoded polypeptide.

Since ribozymes recognize their cognate targets by sequence complementarity, the sequence of a ribozyme that causes a phenotype through its catalytic activity predicts a sequence tag that can be used to clone the target gene. This "Ribozyme Sequence Tag" or RST is 16 bases long, consisting of the two target binding arms (helix 1 and 2) and the requisite GUC in the target (Figure 1A). The RST can thus be used to BLAST search the gene and EST databases, and also can be used as a primer for 3' and 5' RACE. BLASTS of the EST databases yielded several hits, mostly of genes with unknown function. None of the database hits appeared to be related to tumor suppression, cancer or anchorage-dependent growth.

In light of the absence of obvious database hits, the RZ 568 target gene was cloned using the 568 RST as a primer for 5'RACE (Rapid Amplification of cDNA Ends). For 5'RACE, polyA+ mRNA was prepared from HF cells using the Poly(A)Pure kit (Ambion, Austin, TX). The mRNA was used as template for the Marathon cDNA amplification kit (Clontech, Palo Alto, CA). Briefly, a first strand cDNA was synthesized from the mRNA and used

as a template in a second strand synthesis reaction. The ends of the double stranded cDNAs were made blunt with Klenow enzyme and adapters were ligated to the blunt ends. 5' RACE was performed with a primer complementary to the adapters (AP1, 5'CCATCCTAATACGACTCACTATAGGGC3' (SEQ ID NO:11)) and a primer which matches the target recognition site of Rz 568 (5'CGATGCTCCTCTAGACTCGAGGGTACCACCTCCCCGACNCCCT3'(SEQ ID NO:12); the 568 sequence is underlined). The PCR reaction was performed with primer concentrations of 200 nM, AmpliTaq Gold polymerase (Perkin Elmer, Branchburg, NJ) and the following cycle parameters: initial incubation at 94°C for 10 minutes, followed by five 30 second cycles at 94°C, one 4 minute cycle at 68°C; twenty eight 30 second cycles at 94°C, one 30 second cycle at 59°C, one 4 minute cycle at 68°C, and finally one 7 minute cycle at 72°C. The reactions products were gel purified and cloned into a TA cloning vector (Invitrogen, Carlsbad, CA).

Several PCR products were generated from HF mRNA. To verify the presence of a complete 568 target site in these messages, larger gene-specific primers were designed to perform 3'RACE. 3'RACE was performed using HF polyA+ mRNA in a reverse transcription reaction using an anchored polyT-TAG primer (5'GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTV3' (SEQ ID NO:13), where V is either G, A or C) using Superscript reverse transcriptase (GibcoBRL, Rockville, MD) according to the manufacturer's instructions. PCR was performed using a gene specific primer for HTS1 (5'CGGCTCACCGAGATCGGCCC3' (SEQ ID NO:14)) and a primer for the polyT TAG region (5'GGCCACGCGTCGACTAGTACT3' (SEQ ID NO:15)) using the following cycle parameters: initial incubation for 10 minutes at 94°C followed by thirty-five

30 second cycles at 94°C, one 30 second cycle at 55°C, and finally one 4 minute cycle at 72°C. The resulting PCR product was gel purified and cloned into a TA cloning vector.

One of the fragments contained the 568 RST as determined by 3'RACE and sequencing. This cDNA had matches to several incomplete cDNAs in the human EST databases. The deduced amino acid sequence had homology to a *Drosophila* gene, designated peter pan (*ppan*), that was shown to be involved in cell growth, DNA replication and possibly cell-cell communication during development (Migeon et al., Mol. Biol. Cell. 10:1733-1744 (1999); GenBank accession number AF102805))

To clone the rest of HTS1 cDNA, a 20-bp gene-specific primer was used in a 3'RACE, and the 5' and 3' RACE products were ligated together using the common HgaI site. The final ligation product was verified by overlapping sequencing reactions in both directions. The cDNA contains a Kozak ATG translation start site at nucleotide position 103, which is believed to be the start of the protein reading frame due to the fact that a stop codon is present upstream of, and in frame with, this ATG. The region codes for a 473 amino acid protein with a calculated molecular weight of approximately 53 kD. The nucleotide sequence of HTS1 (SEQ ID NO:5) and its predicted amino acid sequence (SEQ ID NO:6), are shown in Figure 6. The nucleotide sequence targeted by Rz 568 is between nucleotides 965 and 979 of the sequence shown in Figure 6A (SEQ ID NO:5), and has the sequence: 5'AGGGCGTCGGGGAGG3' (SEQ ID NO:18).

The HTS1 gene appears to be the homolog of *Drosophila ppan*, and thus has been designated herein hPPAN. This gene appears to be conserved evolutionarily and includes homologs in mouse, *Drosophila*, *C. elegans*, yeast and Arabidopsis. An alignment of hPPAN with homologs from mouse (Mus musculus, compilation of ESTS AI325663, AA756790 and AA575760) and *Drosophila melanogaster* is shown in Figure 3B.

Migeon et al., supra (1999) reported hPPAN and murine PPAN amino acid sequences, based on compilation of EST fragments. The sequences reported by Migeon et al. differ from the sequences obtained from direct cloning of the cDNA. This is most likely due in part to the incompleteness of the available ESTs and their proposed compilation.

EXAMPLE IV

Expression of Human Tumor Suppressor-1 (HTS1)

This example demonstrates the expression of HTS1 (hPPAN) mRNA in Hela and HF cells, and the effect of Rz 568 on HTS1 expression.

To determine if Rz 568 affected the mRNA levels of hPPAN in HF cells, Northern analysis was performed using the full length hPPAN cDNA. Total cellular RNA was prepared using the RNAgents K (Promega, Madison, WI) and 20 µg total RNA was electrophoresed on formaldehyde gels using standard procedures. RNA was transferred to Zeta-Probe membranes (Bio-Rad, Cambridge, MS) by capillary action, as recommended by the manufacturer. Northern hybridizations were performed with QuikHyb (Stratagene, La Jolla, CA) according to their instructions, using the full length hPPAN cDNA random-prime labeled with the High Prime DNA labeling kit

(Boehringer Mannheim, Indianapolis, IN). Northern signals were quantitated by phosphorimager (Molecular Dynamics, Sunnyvale, CA), and data averaged from three to four independent experiments were plotted. hPPAN mRNA levels were normalized to internal G3PDH mRNA and values reported as a percentage, where HF was set to 100%.

Northern blotting identified a single 1.6 kb band. Cells stably expressing Rz 568 consistently showed a 30-35% reduction in hPPAN expression relative to a G3PDH internal control (Figure 3B) while neither d568 nor the unrelated Rz CNR3 had any significant effect on hPPAN mRNA levels. A 10-20% difference in hPPAN levels in Hela vs. HF cells was observed consistently, which implies that hPPAN expression may contribute to the phenotypic differences observed between Hela and HF.

EXAMPLE V

Validation of the role of HTS1 (hPPAN) in anchorage-dependent growth

This example shows that knockdown of HTS1 mRNA by several different ribozymes promotes soft agar colony formation in HF cells, confirming that HTS1 is a tumor suppressor gene.

To confirm that the Rz 568-mediated knockdown of HTS1 (hPPAN) mRNA in HF cells was truly promoting soft agar growth, several other ribozymes were designed against other GUC sites within the hPPAN mRNA. Five "target validation" ribozyme sites were chosen within HTS1. TV 1, 2 and 3 were all located within 150 bases of the 568 Rz site where it was considered that the RNA secondary structure would be sufficiently open and available for cleavage. TV4 and 5 were chosen near the

5' end of the mRNA, at or before the ATG translation start site, which has been shown to often be accessible and vulnerable to ribozyme-mediated cleavage *in vivo*. A ribozyme targeting human immunodeficiency virus was used as a control.

The locations of the target validation ribozyme sites are between nucleotides 3-18 (TV4), 106-121 (TV5), 808-823 (TV1), 866-881 (TV2) and 1163-1178 (TV3) of the nucleotide sequence shown in Figure 6A (SEQ ID NO:5).

The target validation ribozyme genes (as well as control ribozyme genes) were digested with BamHI and MluI and ligated into pLHPM digested with the same enzymes. Each vector contained a different selectable antibiotic marker. Ribozyme sequences were verified by DNA sequencing prior to cell transfections.

Since some Rz may be more active than others, one or two TV Rz genes were stably transfected into HF cells, followed by soft agar selection as described above in Example II. All TV transfections yielded prominent soft agar growth while transfection of a control Rz had no effect (Figure 4A), strongly suggesting that HTS1 was indeed the phenotypically relevant target of the 568 Rz. As further confirmation, three Rz were designed against each of two different (not hPPAN) ESTs of unknown function that came out of a 568 BLAST search. None of those six Rz, alone or in combinations of three, showed any soft agar growth above background. These data further implicate HTS1 in the soft agar phenotype.

Additionally, each of the TV-transfected cell populations, but not the control, showed a reduction in hPPAN mRNA following soft agar selection, as shown in

Figure 4B, thus linking the soft agar phenotype with ribozyme-mediated knockdown of hPPAN.

Under soft agar growth conditions, mechanisms active in HF cells sense their lack of substrate contact and prevent their proliferation, apparently undergoing apoptosis. When Rz 568 reduces the level of hPPAN in these cells, soft agar growth resumes. These results imply that HTS1 is part of a pathway that provides a cell with information about its substrate contact and may be involved in the metastatic potential of transformed cells.

EXAMPLE VI

Effect of overexpression of HTS1

This example shows that overexpression of HTS1 prevents Hela cell growth.

If HTS1 (hPPAN) was indeed involved in preventing HF growth in soft agar, it was hypothesized that overexpression of HTS1 in transformed Hela cells should block their ability to grow in soft agar. To test this hypothesis, the wild type HTS1 and a frameshift mutant of HTS1 were expressed in both Hela and HF cells under the control of the CMV promoter. In this plasmid, the CMV transcript is designed to be bicistronic with the ECMV IRES initiating translation of the hygromycin resistance gene. Therefore, resistance to hygromycin indicates expression of HTS1 cDNA as well.

To create the frameshift (FS) mutant of HTS1, the unique BssHII site at nucleotide position 135 (amino acid 12) was digested and the overhanging ends were filled in with Klenow polymerase. The resulting blunt

ends were re-ligated, thus shifting the coding frame by 1 base. The frameshift was verified by DNA sequencing and this new reading frame continues for 53 amino acids before a translation stop.

Expression of HTS1 (hPPAN) or the corresponding frameshift mutation (FS) had no effect on the growth of HF cells compared to the vector alone, as determined by the number of stable hygromycin resistant colonies following transfection and selection (Figure 5, left panels). However, expression of the wild type hPPAN in Hela cells resulted in a sharp decrease in the number of hygromycin-resistant colonies as compared to its frameshifted control (Figure 5, right panels). This inability to select stable hPPAN expressing cells preventing testing the hypothesis that hPPAN would block Hela soft agar growth. Indeed, overexpression of hPPAN appears to block all Hela cell growth.

These results suggest that endogenous HTS1 (hPPAN) may not signal when the cell is on an inappropriate substrate, perhaps due to additional regulators downstream. Overexpression of hPPAN may override this control, sending a constitutive signal that the cell is on an inappropriate substrate. hPPAN-induced death in Hela cells may be via an apoptotic pathway or some type of cell cycle arrest.

Throughout this application various publications and database Accession numbers have been referenced. The disclosures of these publications and Accession number nucleotide and amino acid sequences, in their entireties, are hereby incorporated by reference in this application in order to more fully describe the state of the art to which this invention pertains.

Although the invention has been described with reference to the disclosed embodiments, those skilled in the art will readily appreciate that the specific experiments detailed are only illustrative of the invention. It should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.